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RAW SEQUENCE LISTING

DATE: 11/18/2002
TIME: 13:03:07

PATENT APPLICATION: US/09/988,013A

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\11182002\I988013A.raw

3 <110> APPLICANT: LEUNG, Shui-on
4 HANSEN, Hans
6 <120> TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
7 CELL LYMPHOMA AND LEUKEMIA CELLS
9 <130> FILE REFERENCE: 18733/1082
11 <140> CURRENT APPLICATION NUMBER: US 09/988,013A
C--> 12 <141> CURRENT FILING DATE: 2002-10-29
14 <150> PRIOR APPLICATION NUMBER: US 09/741,843
15 <151> PRIOR FILING DATE: 2000-12-22
17 <150> PRIOR APPLICATION NUMBER: US 09/127,902
18 <151> PRIOR FILING DATE: 1998-08-03
20 <150> PRIOR APPLICATION NUMBER: US 08/690,102
21 <151> PRIOR FILING DATE: 1996-07-06
23 <150> PRIOR APPLICATION NUMBER: US 08/289,576
24 <151> PRIOR FILING DATE: 1994-08-12
26 <160> NUMBER OF SEQ ID NOS: 25
28 <170> SOFTWARE: PatentIn version 3.1
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33 <213> ORGANISM: Murinae gen. sp.
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37 <222> LOCATION: (1)..(339)
38 <223> OTHER INFORMATION:
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43 1 5 10 15
45 gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
46 Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
47 20 25 30
49 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144
50 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
51 35 40 45
53 tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
54 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
55 50 55 60
57 cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 240
58 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
59 65 70 75 80
61 atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa 288
62 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln

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DATE: 11/18/2002

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65 tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa      336
66 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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69 cgt      339
70 Arg
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86          20          25          30
89 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
90          35          40          45
93 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
94          50          55          60
97 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
98 65          70          75          80
101 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
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126 1          5          10          15
128 tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac      96
129 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
130          20          25          30
132 tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att      144
133 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
134          35          40          45
136 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc      192
137 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
138          50          55          60
140 aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac      240
141 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

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142 65          70          75          80
144 atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt      288
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146          85          90          95
148 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc      336
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150          100          105          110
152 aca gtc tcc tcg      348
153 Thr Val Ser Ser
154          115
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159 <212> TYPE: PRT
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165 1          5          10          15
168 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
169          20          25          30
172 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
173          35          40          45
176 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
177          50          55          60
180 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
181 65          70          75          80
184 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
185          85          90          95
188 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
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211 gat agg gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt      96
212 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
213          20          25          30
215 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg aaa      144
216 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
217          35          40          45

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219 gca cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc      192
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221      50                      55                      60
223 cct tcg cga ttc tct ggc agc gga tct ggg aca gat ttt act ttc acc      240
224 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
225 65                      70                      75                      80
227 atc agc tct ctt caa cca gaa gac att gca aca tat tat tgt cac caa      288
228 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
229                      85                      90                      95
231 tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag gtg cag atc aaa      336
232 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
233      100                      105                      110
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236 Arg
240 <210> SEQ ID NO: 6
241 <211> LENGTH: 113
242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens
245 <400> SEQUENCE: 6
247 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
248 1                      5                      10                      15
251 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
252      20                      25                      30
255 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
256      35                      40                      45
259 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
260      50                      55                      60
263 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
264 65                      70                      75                      80
267 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
268      85                      90                      95
271 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
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275 Arg
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280 <211> LENGTH: 348
281 <212> TYPE: DNA
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287 <223> OTHER INFORMATION:
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292 1                      5                      10                      15
294 tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac      96
295 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
296      20                      25                      30

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Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\11182002\I988013A.raw

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298 tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att      144
299 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
300      35      40      45
302 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc      192
303 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
304      50      55      60
306 aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac      240
307 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
308 65      70      75      80
310 atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt      288
311 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
312      85      90      95
314 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc      336
315 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
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319 Thr Val Ser Ser
320      115
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328 <400> SEQUENCE: 8
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334 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
335      20      25      30
338 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
339      35      40      45
342 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
343      50      55      60
346 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
347 65      70      75      80
350 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
351      85      90      95
354 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
355      100      105      110
358 Thr Val Ser Ser
359      115
362 <210> SEQ ID NO: 9
363 <211> LENGTH: 116
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365 <213> ORGANISM: Homo sapiens
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370 1      5      10      15
373 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
374      20      25      30
377 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

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VERIFICATION SUMMARY

DATE: 11/18/2002

PATENT APPLICATION: US/09/988,013A

TIME: 13:03:09

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L:123 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:121
L:206 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:204
L:289 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:287